## Construction of Broad-Host-Range Plasmid Vectors for Easy Visible Selection and Analysis of Promoters

MARK A. FARINHA AND ANDREW M. KROPINSKI\*

Department of Microbiology and Immunology, Queen's University, Kingston, Ontario, Canada K7L 3N6

Received 15 November 1989/Accepted 9 March 1990

We have constructed a series of broad-host-range plasmids which use "visual screens" to detect promoter activity. These plasmids contain the pMB1 and pRO1600 origins of replication and are capable of replicating in a wide range of gram-negative bacteria. The genes encoding β-galactosidase and alkaline phosphatase from Escherichia coli and bacterial luciferase from Vibrio harveyi supply the promoterless indicator genes. The constructs were tested in E. coli and Pseudomonas aeruginosa.

The lack of versatile small plasmid vectors for use in Pseudomonas spp. led us to construct a set of plasmids for general cloning and promoter selection in *Pseudomonas* spp. and Escherichia coli (9). These were based on the pRO1600 replicon, which can be maintained in a wide variety of gram-negative bacteria (18). Promoter selection was dependent on cloning DNA sequences upstream of promoterless tetracycline (tetA) (6) and chloramphenicol (cat) (23) antibiotic resistance genes. These vectors have been used to clone promoters from Pseudomonas aeruginosa bacteriophages φPLS27 (1, 9) and D3 (10, 14; M. A. Farinha, B. J. Allan, S. Ronald, and A. M. Kropinski, Abstr. Annu. Meet. Am. Soc. Microbiol. 1989, H-114, p. 188) and also to dissect the promoters of the regA gene, which controls the expression of exotoxin A in P. aeruginosa (D. Storey, personal communication). The use of antibiotic resistance for promoter selection has proven difficult in several respects. The selection of weak or temporally regulated promoters is tricky, since the cells often do not survive the antibiotic challenge. Furthermore, the need to use high concentrations of antibiotics when working with *Pseudomonas* spp. also limits the utility of these constructs. Finally, the expense and limited sensitivity of available assay systems for quantitating promoter activity are major drawbacks in using these vectors.

This article introduces a new series of promoter selection plasmids which have been developed to overcome the problems of the first-generation constructs. They utilize promoterless lacZ ( $\beta$ -galactosidase) and phoA (alkaline phosphatase) genes from  $E.\ coli$  and the luxAB (luciferase) genes from  $Vibrio\ harveyi$ . The activities of the products of these genes can be visually assayed with a high degree of sensitivity and accuracy (3, 13, 16).

Construction of plasmids. pQF40 is a tetracycline promoter-probe vector derived from pQF10, a deletion derivative of pRO1614 (9, 18). This plasmid was used as the basic replicon for constructing pQF50 (lacZ), pQF60 (phoA), and pQF70 (luxAB).

pQF50 utilizes the promoterless lacZ gene derived from pCB267 (21). In the latter construct, the first 15 bases of the lacZ gene have been replaced with the Shine-Dalgarno sequence and the first 12 bases of the  $E.\ coli$  lipoprotein (lpp) gene (12, 17, 20). This region also contains translational stop codons in all three reading frames. The hybrid  $\beta$ -galactosidase is enzymatically indistinguishable from the native pro-

pQF60 was constructed by using the promoterless alkaline phosphatase (phoA) gene from pCB267 (7, 21). The alkaline phosphatase gene was transferred first to pBR322 and then to pQF40, replacing the promoterless tetA gene.

pQF70 was similarly created by using the luciferase (luxAB) genes taken from pLAV1, which was a gift from T. Baldwin (personal communication). The luxAB genes were first transferred to pBR322 and then to pQF40, replacing the promoterless tetracycline gene (Fig. 2).

Testing of promoter-probe vectors. All three vectors were linearized within the multiple-cloning region at a unique BamHI restriction site, using enzyme and buffers purchased from Gibco/BRL Canada (Burlington, Ontario, Canada). An electroelution-purified 665-base-pair Sau3A restriction digest fragment from pBR322, containing the divergently arranged tetA/tetR promoters (2), was ligated into the linearized vectors. Insertion of the Sau3A fragment in either orientation should therefore activate the promoterless genes. Ligated plasmids were transformed into E. coli JM106 (25) by the method described by Maniatis et al. (15) and into P. aeruginosa OT684 (19) by the method described by Berry and Kropinski (4). All clones were selected on plates containing tryptic soy broth (Difco Laboratories, Detroit, Mich.)-supplemented agar (15 g/liter) and with either 150 µg of ampicillin or 300 µg of carbenicillin per ml for selection in E. coli and P. aeruginosa, respectively. The chromogenic substrates 5-bromo-4-chloro-3-indolyl-β-D-galactopyrano-

tein, which is 1 amino acid longer than the hybrid enzyme. To facilitate cloning, the upstream region of lacZ has been further modified to contain a large multiple-cloning site derived from pUC18 (25) and pMTL20 (S. P. Chambers, D. A. Barstow, and N. P. Minton, Abstr. Int. Congr. Microbiol. 1986, P.13-12, p. 199). An artificial trpA terminator was synthesized and inserted upstream of the multiple-cloning site but was insufficient to prevent readthrough from promoters located in the pBR322 region of the plasmid. A second synthetic trpA terminator [Pharmacia (Canada) Inc., Baie d'Urfe, Quebec, Canada] was inserted in tandem with the other terminator at the unique NruI site. The latter was created as a result of the addition of the first terminator. This arrangement proved successful in eliminating readthrough transcription. The sequence from the beginning of the lacZ gene upstream through the synthetic terminators was confirmed by double-stranded dideoxy sequencing with the universal primer (24) and Sequenase (United States Biochemical Corp., Cleveland, Ohio) (Fig. 1).

<sup>\*</sup> Corresponding author.

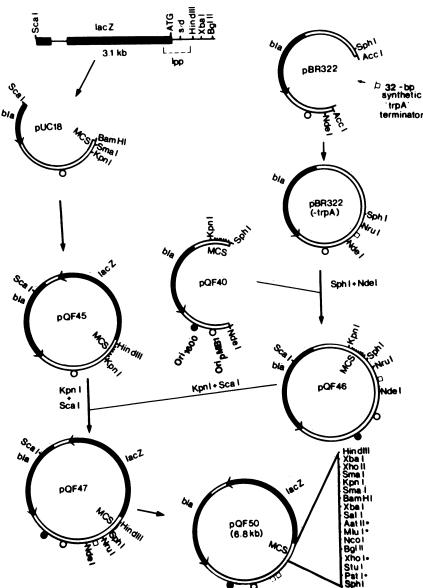


FIG. 1. The lacZ gene from pCB267 was excised as a 3.1-kilobase BgIII-ScaI fragment and ligated into pUC18 cut with BamHI-ScaI, creating pQF45. The BamHI-BgIII fusion creates a new XhoII site. A 32-base-pair trpA transcription terminator,

## 5'-CGCGAAAAAAAGCCCGCTCATTAGGCGGGCT GCTTTTTTCGGGCGAGTAATCCGCCCGATA-5'

was synthesized and inserted into pBR322 cut with AccI. This insertion created a new NruI site. The terminator was then transferred to pQF40 as a SphI-NdeI fragment, creating pQF46. The lacZ gene from pQF45 was then transferred to pQF46 as a KpnI-ScaI fragment, creating pQF47. On testing pQF47 in  $E.\ coli$ , a low level of  $\beta$ -galactosidase activity was detectable. To alleviate this problem a second synthetic trpA terminator was installed in tandem next to the first by blunt-end ligation into the NruI site. This created the 6.8-kilobase vector pQF50. \*, Nonunique restriction sites in the multiple-cloning site.

side (X-Gal) (Gibco/BRL) and 5-bromo-4-chloro-3-indolyl phosphate (Sigma Chemical Co., St. Louis, Mo.) were added to the media at 20 and 40 μg/ml, respectively. Promoterpositive clones of pQF50 (lacZ) and pQF60 (phoA) manifested themselves as blue colonies. Luciferase-positive clones of pQF70 (luxAB) were detected by swabbing the inside of the petri dish lid with n-decanal (Sigma). This volatile long-chain aldehyde is utilized along with oxygen and FMNH by bacterial luciferase to produce a blue-green light that can be detected in a darkened room or by brief exposure to X-ray film (22). Positive and negative clones

from all three constructs were screened for the 665-base-pair insert by mini-preps (5) and by digestion with Sau3A. Positive clones showed the insert, while negative clones revealed only religated vector without any insert. The orientations of the inserts were also determined by restriction endonuclease digestion. Clones demonstrating both promoter orientations were chosen from each plasmid type for  $E.\ coli$  and  $P.\ aeruginosa$  and subsequently assayed quantitatively for the activity of the reporter gene product. Assays for  $\beta$ -galactosidase were carried out with o-nitrophenol- $\beta$ -D-galactopyranoside substrate (Sigma) as described by

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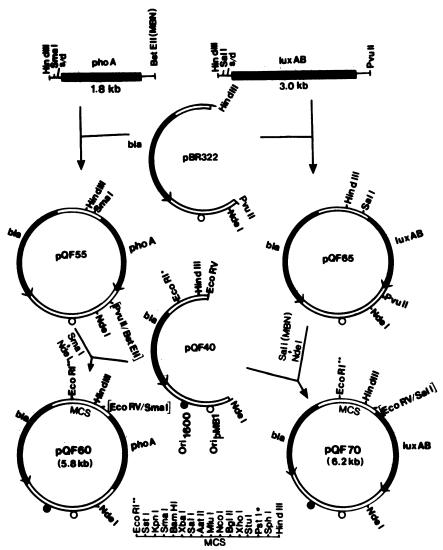


FIG. 2. The 1.8-kilobase alkaline phosphatase gene from pCB267 was recovered by digestion with BstEII (rendered blunt with mung bean nuclease [MBN]) and HindIII. This was then ligated to pBR322 cut with HindIII-PvuII, creating pQF55. The [PvuII/BstEII] fusion destroyed both restriction sites. The phoA gene was then transferred as a SmaI-NdeI fragment to pQF40 cut with EcoRV-NdeI, creating the final product, pQF60, which is 5.8 kilobases and contains a large multiple-cloning site (MCS). EcoRI\*\* indicates the presence of a T1 transcription terminator (6) which prevents readthrough from upstream promoters into the phoA gene. The 3.0-kilobase luciferase gene (luxAB) was excised from pLAV1 as a HindIII-PvuII fragment and ligated into pBR322 cut with HindIII-PvuII, creating pQF65. The luxAB genes were then transferred from pQF65 by digestion with SaII (rendered blunt with mung bean nuclease) and NdeI to pQF40 cut with EcoRV-NdeI. This created the final product, pQF70, which is 6.2 kilobases and has the same multiple-cloning site as pQF60. \*, Nonunique restriction sites in the multiple-cloning site.

Miller (16), except that cells were broken by sonication (60 s on ice) instead of by permeabilization with toluene. Alkaline phosphatase activity was measured by using p-nitrophenol phosphate substrate (Sigma) as described by Kreuzer et al. (13) by using whole cells grown in phosphate-rich medium (LB plus 2 mM  $K_2HPO_4$ ) to repress chromosomal alkaline phosphatase production. Luciferase was assayed using sonicated cell extracts and the buffer systems described by Baldwin et al. (3). Luminescence was quantitated with a scintillation counter (RackBeta; LKB Instruments, Inc., Rockville, Md.) set in the chemiluminescence detection mode. The activity of the culture was reported in the units described by Engebrecht et al. (8).

The data presented in Table 1 are comparable to results previously reported for the tetA/tetR promoter element from

pBR322 (7, 21). The approximately twofold-greater strength of tetR over tetA is apparent in both E. coli and P. aeruginosa when all three reporter gene systems are used. Additionally, the values obtained for E. coli and P. aeruginosa are comparable when the copy number difference is taken into account. The copy number remained unchanged from the previously reported values of approximately 13 in P. aeruginosa and 36 in E. coli (9).

The vectors described are suitable for the detection and analysis of promoters in a wide range of gram-negative bacteria. Comparisons of promoter strength in different hosts are also possible. All the vectors have translational stop codons in all three reading frames located between the multiple-cloning site and the translation initiation codon of the indicator gene. This prevents initiation of transcription

TABLE 1. Expression of reporter genes phoA, lacZ, and luxAB in promoter selection v	ectors under the control
of the tetA and tetR promoters	

Host strain and relevant genotype	Promoter <sup>a</sup>	Sp act		
		β-Galactosidase <sup>b</sup> (pQF50)	Alkaline phosphatase <sup>c</sup> (pQF60)	Luciferase <sup>d</sup> (pQF70)
E. coli JM106 (phoA+ lacZ)	None	<1	5	8
	tetA	85	98	446
	tetR	195	202	1,371
P. aeruginosa OT684 (phoA <sup>+</sup> lacZ)	None	1	1	2
	tetA	35	38	215
	tetR	60	79	640

<sup>a</sup> Promoter with which gene was aligned.

<sup>b</sup> Expressed in Miller units (16).

<sup>c</sup> Expressed in units as defined by Kreuzer et al. (13).

<sup>d</sup> Expressed in relative light units as described by Engebrecht et al. (8).

from other start sites into the indicator gene, which may have detrimental effects on its expression. These plasmids, like their predecessors pQF26 and pQF40 (9), are extremely stable even in the absence of antibiotic selection pressure.

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